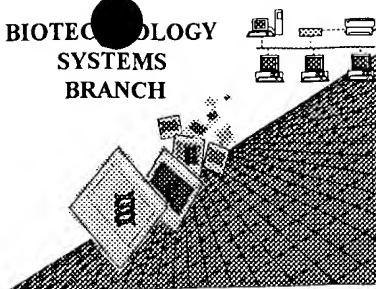


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,395
Source: PCR 09
Date Processed by STIC: 1/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/673,395

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
 TIME: 11:53:49

Input Set : N:\COPIES\ES.txt
 Output Set: N:\CRF3\01232001\I673395.raw

4 <110> APPLICANT: metaGen Gesellschaft fur Genomforschung mbH (Assignec)
 6 <120> TITLE OF INVENTION: Human Nucleic Acid Sequences from Uterus Tumor Tissue
 8 <130> FILE REFERENCE: 51586AWOMLXX24-P
 10 <140> CURRENT APPLICATION NUMBER: US/09/673,395
 11 <141> CURRENT FILING DATE: 2000-10-17
 13 <160> NUMBER OF SEQ ID NOS: 635

pg 1-4

Does Not Comply
 Corrected Diskette Needed
 do not use foreign accent marks; they do not
 translate
 in the CRF
 program

ERRORRED SEQUENCES

14671 <210> SEQ ID NO: 494
 14672 <211> LENGTH: 85
 14673 <212> TYPE: PRT
 14674 <213> ORGANISM: homo sapiens
 14676 <400> SEQUENCE: 494
 14678 Lys Gly Ser Leu Pro Pro Thr Lys Gln Gly Lys Leu Gly Gln Leu Ala
 14679 1 5 10 15
 14681 Pro Gly His Gln Gly Gln Leu Pro Thr Trp Leu Leu Pro Phe Leu Gly
 14682 20 25 30
 14684 Phe Phe Gln Gly Phe Gly Asn Ser Leu Gly Val Gly Glu Val Ala Ser
 14685 35 40 45
 14687 Cys Leu His Trp Tyr Trp Pro Arg Arg Trp Ala Gly His Gly Gly Gly
 14688 50 55 60
 14690 Gly Val Asn Ile Trp Phe Ile Ser His Pro Ala Gly Cys Lys Pro Leu
 14691 65 70 75 80

E--> 14693 val Lys

17275 <210> SEQ ID NO: 573
 17276 <211> LENGTH: 91
 17277 <212> TYPE: PRT
 17278 <213> ORGANISM: homo sapiens
 17280 <400> SEQUENCE: 573

17282 Asp Ser Gln Val Gly Arg Gly Pro Gln Arg Asn Ser Ser Leu His Thr
 17283 1 5 10 15
 17285 Gly Arg Ser Val His Trp Gly Glu Ala Thr Gly Ser Leu Arg His Leu
 17286 20 25 30
 17288 Gln Trp Gly Arg Ala Gln Pro Leu Leu Phe Leu Gly Gly Lys Leu Arg
 17289 35 40 45
 E--> 17291 Phe Lys Leu Pro Gly Gly Lys Ser Met Gly Arg Lys Gln Ala Leu
 17292 50 55 60
 17294 Leu Leu Arg Val Ser Val Ser Pro Phe Phe Pro Leu Cys Leu Ile Asn
 17295 65 70 75 80
 17297 Lys Phe His Phe Ser His Pro Ser Asn Ser Leu
 17298 85 90

17300 <210> SEQ ID NO: 574
 17301 <211> LENGTH: 89
 17302 <212> TYPE: PRT
 17303 <213> ORGANISM: homo sapiens

Please
 consult
 new sequence
 rules for
 valid format.

Per new sequence
 rules, use Xaa AND
 explain in 2227-2237
 use Xaa section

(see item 10
 on Erra
 summary sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:53

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

17305 <400> SEQUENCE: 574
17307 Glu Lys Trp Asn Leu Leu Ile Arg His Lys Gly Lys Lys Gly Glu Thr
17308 1 5
E--> 17310 Glu Thr Leu Ser Lys **Xxx** Arg Ala Cys Phe Leu Pro Met Asp Phe Pro
17311 20 25 30
17313 Pro Gly Ser Leu Asn Arg Ser Phe Pro Arg Lys Arg Arg Gly Trp
17314 35 40 45
17316 Ala Leu Pro His Trp Arg Trp Arg Lys Leu Pro Val Ala Ser Pro Gln
17317 50 55 60
17319 Cys Thr Leu Leu Pro Val Cys Arg Leu Glu Phe Leu Trp Gly Pro Leu
17320 65 70 75 80
17322 Pro Thr Trp Leu Ser His Cys Pro Leu
17323 85
17351 <210> SEQ ID NO: 577
17352 <211> LENGTH: 161
17353 <212> TYPE: PRT
17354 <213> ORGANISM: homo sapiens
17356 <400> SEQUENCE: 577
E--> 17358 Leu Leu Pro Leu Leu Leu Leu Ile His Gly Asp Thr Pro **Xxx** Gly
17359 1 5 10
E--> 17361 Pro Gly Pro **Xxx** **Xxx** Gln Glu Gln Ala Pro Asn His Arg His Gly Leu
17362 20 25 30
E--> 17364 Glu Glu **Xxx** Arg Ile Ser **Xxx** Lys Ser Cys Met Gly **Xxx** Val Asp Trp
17365 35 40 45
17367 Asn Gly Pro Glu Gly Val Glu Ile Tyr Val Asp Gly Lys Glu Pro His
17368 50 55 60
E--> 17370 Asn Lys Ser Gln Ser Ser Gln Leu Gly Phe Lys Thr Asn Gly His **Xxx**
17371 65 70 75 80
E--> 17373 Lys Ser Ser Glu **Xxx** Val **Xxx** His Asp Val Leu Asp Asn Arg Lys Glu
17374 85 90 95
17376 Ala Gly Val Lys Val Lys Glu Gly His Glu His Gln Asn Gln Gln Asp
17377 100 105 110
17379 Pro Ala Ser Glu Leu His Val Leu Phe Gly Gly Ala Leu Thr His Gly
17380 115 120 125
17382 Gly Asp Ala Arg Lys His Ala Leu Pro Phe Arg Thr Gly Phe Ser Arg
17383 130 135 140
17385 Ser Thr Gln Gln Pro Pro Arg Ala Arg Phe Leu Pro Leu Cys Arg
17386 145 150 155 160
17388 Thr
17390 <210> SEQ ID NO: 578
17391 <211> LENGTH: 160
17392 <212> TYPE: PRT
17393 <213> ORGANISM: homo sapiens
17395 <400> SEQUENCE: 578
E--> 17397 Gln Thr Asp Asn Leu Ser Glu Arg Gln Pro **Xxx** Gly Lys **Xxx** Val Cys
17398 1 5 10 15
17400 Arg Gly Cys Pro Gln Gly Glu Cys Ser Trp Glu Arg Ala Val Leu Leu
17401 20 25 30
E--> 17403 **Xxx** Pro Gly Arg Pro Ala Leu Ser **Xxx** Thr Leu Leu **Xxx** Lys **Xxx** Ala

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
 TIME: 11:53:53

Input Set : N:\COPIES\ES.txt
 Output Set: N:\CRF3\01232001\I673395.raw

```

17404      35
E--> 17406   Pro  Cys  Glu  Val  Asn  Trp  Val  Xxx  Val  Arg  Gly  Ser  Xxx  Xxx  Cys  Xxx
17407      50
E--> 17409   Gly  Ala  Pro  Ala  Xxx  Thr  Pro  Xxx  Pro  Xxx  Gln  Arg  Xxx  Ala  Ala  Ser
17410      65
E--> 17412   Ala  Xxx  Ala  Gly  Leu  Glu  Xxx  Ser  Xxx  Ala  Xxx  Ala  Gly  Xxx  Ala  Gly
17413      85
E--> 17415   Cys  Cys  Cys  Xxx  Gly  Leu  Pro  Xxx  Val  Trp  Ser  Xxx  Leu  Ala  Leu  Pro
17416     100
E--> 17418   Thr  Ala  Ser  Leu  Glu  Ala  Ser  Xxx  Xxx  Pro  Arg  Pro  Ala  Ala  Ser  Pro
17419     115
17421   Arg  Thr  Ser  Cys  Pro  Ser  Thr  Leu  Pro  Gln  Ala  Thr  Lys  Thr  Pro  Arg
17422     130
E--> 17424   Val  Leu  Pro  Asn  Lys  Xxx  Xxx  Leu  Gly  Thr  Xxx  Ser  Lys  Leu  Ile  Phe
17425     145
18471 <210> SEQ ID NO: 603
18472 <211> LENGTH: 163
18473 <212> TYPE: PRT
18474 <213> ORGANISM: homo sapiens
18476 <400> SEQUENCE: 603
18478   Ile  Tyr  Gly  Val  Ser  Phe  Leu  Ile  Phe  Asn  Ile  Lys  Asn  Ile  Tyr  Val
18479      5
18481   Ser  Val  Ile  Pro  Cys  Gln  Gly  Cys  Leu  Val  Cys  Leu  Arg  Phe  Cys
18482     20
18484   Phe  Ile  Phe  Ile  His  Val  Val  Val  Ile  Phe  Ser  Ser  Gln  Phe  Leu  Leu
18485     35
18487   Val  Ser  Pro  Phe  Pro  Gly  Ser  Phe  Leu  Leu  Leu  Leu  Ser  Val  Gly
18488     50
18490   Asp  Asp  Lys  Leu  Val  Ser  Leu  Arg  Ala  Leu  His  Leu  Trp  Ile  Phe  Leu
18491     70
E--> 18493   Xxx  Ser  Leu  Thr  Gly  Gln  Pro  Ala  Pro  Val  Gly  Ser  Gly  Pro  Val  Leu
18494     85
E--> 18496   Arg  Leu  Pro  Arg  Ser  Leu  Phe  His  Leu  Gln  Val  Cys  Leu  Pro  Xxx  Pro
18497     100
18499   Ala  Pro  Gly  Leu  Ala  Pro  Ala  Ala  Ala  Cys  Pro  Ser  Glu  Ala  Leu  Leu
18500     115
18502   Ser  Pro  Pro  Gly  Ser  His  Gly  Trp  Phe  Pro  Leu  Ser  Gln  Leu  Val  Ser
18503     130
18505   Leu  Asn  Pro  Lys  Pro  Leu  Arg  Asn  Trp  Gly  Leu  Val  Ser  Gly  Thr  Cys
18506     145
18508   Cys  Tyr  Gln
18510 <210> SEQ ID NO: 604
18511 <211> LENGTH: 150
18512 <212> TYPE: PRT
18513 <213> ORGANISM: homo sapiens
18515 <400> SEQUENCE: 604
18517   Pro  Leu  Ser  Phe  Leu  Met  Tyr  Lys  Thr  Leu  Leu  Ser  Gly  Leu  Gln  Phe
18518      1
E--> 18520   Glu  His  Leu  Trp  Xxx  Phe  Ile  Tyr  Phe  Ala  Xxx  Val  Cys  Gly  Gln  Ser

```

same

same

same

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
 TIME: 11:53:53

Input Set : N:\COPIES\ES.txt
 Output Set: N:\CRF3\01232001\I673395.raw

```

18521
E--> 18523 Asn Ile Phe 20 Pro Lys Tyr Ile Leu 25 Arg Lys Xxx Lys Lys Gln Ile
18524 35 40 45
E--> 18526 Arg Xxx Phe Asp Xxx Lys Xxx Asn Arg Pro Xxx Lys Gly Ala Xxx Thr
18527 50 55 60
E--> 18529 Trp Ser Arg Ala Trp Xxx Arg Gly Lys Ala Xxx Arg Gly Gln Val Cys
18530 65 70 75 80
E--> 18532 Cys Gly Gln Ile Cys Ala Tyr Phe Ile Thr Gly Val Lys Xxx Lys Gln
18533 85 90 95
E--> 18535 Ser Xxx Ile Asp Val Xxx Arg Ile Tyr Thr Val Xxx Arg Asn Xxx Arg
18536 100 105 110
E--> 18538 Xxx Xxx Phe Xxx Lys Asn Arg Asn Thr Xxx Trp Xxx Xxx Phe Tyr His
18539 115 120 125
E--> 18541 Xxx Xxx Tyr Thr Phe Ser Leu Trp Xxx Asn Xxx Leu Thr Lys Leu Xxx
18542 130 135 140
18544 Phe Lys Ile Lys Leu Met
18545 145 150
19593 <210> SEQ ID NO: 635
19594 <211> LENGTH: 89
19595 <212> TYPE: PRF
19596 <213> ORGANISM: homo sapiens
19598 <400> SEQUENCE: 635
19600 Phe Ile Gln Phe Ser Arg Pro Gly Ser Pro Leu Ser Leu Asp Gly Leu
19601 1 5 10 15
E--> 19603 Ser Xxx Ala Ile Ala Ser Cys Xxx Leu Asn His Thr Ala Asn Pro Thr
19604 20 25 30
19606 Ser Asn Ser Asn Phe Leu Asp Leu Asn Leu Pro Pro Gln His Asn Thr
19607 35 40 45
19609 Gly Leu Gly Gly Ile Pro Val Ala Gly Glu Glu Glu Val Lys Val Ser
19610 50 55 60
19612 Thr Met Pro Leu Ser Thr Ser Ser His Ser Leu Gln Gln Gly Gln Gln
19613 65 70 75 80
19615 Pro Thr Ser Leu His Thr Thr Val Ala
19616 85
E--> 19626 276
E--> 19628 265
E--> 19632 295
E--> 19635 312

```

same

same

delete at end of file

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001

TIME: 11:53:54

Input Set : N:\COPIES\ES.txt

Output Set: N:\CRF3\01232001\I673395.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2151 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:79
L:2151 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:79
L:2151 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:79
L:11033 M:283 W: Missing Blank Line separator, <400> field identifier
L:11034 M:300 W: (50) Intentionally skipped Sequence, : Sequence id (359) SEQUENCE:
L:14693 M:252 E: No. of Seq. differs, <211>LENGTH:Input:83 Found:82 SEQ:494
L:15633 M:283 W: Missing Blank Line separator, <400> field identifier
L:15634 M:300 W: (50) Intentionally skipped Sequence, : Sequence id (529) SEQUENCE:
L:15637 M:283 W: Missing Blank Line separator, <400> field identifier
L:15638 M:300 W: (50) Intentionally skipped Sequence, : Sequence id (530) SEQUENCE:
L:15812 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:535
L:15812 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:535
M:340 Repeated in SeqNo=535
L:15839 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15839 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
M:340 Repeated in SeqNo=536
L:15841 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:54

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

L:15845 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:16273 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:545
M:340 Repeated in SeqNo=545
L:16488 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:550
M:340 Repeated in SeqNo=550
L:16573 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:552
M:340 Repeated in SeqNo=552
L:16604 M:283 W: Missing Blank Line separator, <400> field identifier
L:16605 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (553) SEQUENCE:
L:16654 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:555
L:16663 M:283 W: Missing Blank Line separator, <400> field identifier
L:16664 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (556) SEQUENCE:
L:16667 M:283 W: Missing Blank Line separator, <400> field identifier
L:16668 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (557) SEQUENCE:
L:16671 M:283 W: Missing Blank Line separator, <400> field identifier
L:16672 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (558) SEQUENCE:
L:16675 M:283 W: Missing Blank Line separator, <400> field identifier
L:16676 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (559) SEQUENCE:
L:16679 M:283 W: Missing Blank Line separator, <400> field identifier
L:16680 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (560) SEQUENCE:
L:17291 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17310 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17348 M:283 W: Missing Blank Line separator, <400> field identifier
L:17349 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (576) SEQUENCE:
L:17358 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17361 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17364 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:17370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17373 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17397 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17403 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17406 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17409 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17412 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5

VERIFICATION SUMMARY

DATE: 01/23/2001

PATENT APPLICATION: US/09/673,395

TIME: 11:53:54

Input Set : N:\COPIES\ES.txt

Output Set: N:\CRF3\01232001\I673395.raw

L:17415 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:17418 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:17424 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:18493 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:18496 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:18520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:18523 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:18526 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
 L:18529 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:18532 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:18535 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:18538 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
 L:18541 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
 L:18554 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:18557 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
 L:18560 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:18563 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:18566 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:18569 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
 L:18572 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19049 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19052 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19058 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:19061 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19067 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19079 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19089 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:19165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19168 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:19174 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:19177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19180 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:19183 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19367 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19407 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19419 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19423 M:283 W: Missing Blank Line separator, <400> field identifier
 L:19424 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (626) SEQUENCE:
 L:19427 M:283 W: Missing Blank Line separator, <400> field identifier
 L:19428 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (627) SEQUENCE:
 L:19431 M:283 W: Missing Blank Line separator, <400> field identifier
 L:19432 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (628) SEQUENCE:
 L:19435 M:283 W: Missing Blank Line separator, <400> field identifier
 L:19436 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (629) SEQUENCE:
 L:19562 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19565 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:19626 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:635
 M:332 Repeated in SeqNo=635